

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Evans, Ronald M.
No, David

(ii) TITLE OF INVENTION: HORMONE-MEDIATED METHODS FOR MODULATING
EXPRESSION OF EXOGENOUS GENES IN MAMMALIAN SYSTEMS, AND
PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gray-Cary Ware & Freidenrich LLP
(B) STREET: 4365 Executive Drive, Suite 1600
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92121-2189

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/974,530
(B) FILING DATE: November 19, 1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E.
(B) REGISTRATION NUMBER: 31,192
(C) REFERENCE/DOCKET NUMBER: SALK1520-2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-677-1409
(B) TELEFAX: 619-677-1465

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
1      5      10      15

Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
      20      25      30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      35      40      45

Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
      50      55      60

Lys Cys Xaa Xaa Xaa Gly Met
65      70

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Glu Gly Cys Lys Gly
1      5

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ser Cys Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..2241
(D) OTHER INFORMATION: /product= "VgEcR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GCC CCC CCG ACC GAT GTC AGC CTG GCG GAC GAG CTC CAC TTA GAC	48
Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp	
1 5 10 15	
GCG GAG GAC CTC CCG ATG CCG CAT GCG GAC CCG CTA GAC GAT TTC GAT	96
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp	
20 25 30	
CTG CAC ATG TTG GCG GAG GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC	144
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro	
35 40 45	
CAC GAC TCC GCC CCC TAC GCG GCT CTG GAT ATG GCG GAC TTC GAG TTT	192
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe	
50 55 60	
GAG CAG ATG TTT ACC GAT GCC CTT GGA ATT GAC GAG TAC GGT CCG AAG	240
Glu Glu Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys	
65 70 75 80	
CTT CTA GGT ACC TCT ACA AGC ATA TCG AAT TCT ATA TCT TCA GGT CCG	288
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg	
85 90 95	
GAT GAT CTC TCG CCT TCG AGC AGC TTG AAC GGA TAC TCG CCG AAC GAA	336
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu	
100 105 110	
AGC TCG GAT CCG AAG AAG AGC AAG AAG GGA CXT GCG CCA CCG CTC CAA	384
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Glu	
115 120 125	

GAG GAG CTC TGC CTC GTT TGC GGC GAC AGG GCC TCC GGC TAC CAC TAC 432
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

AAC GCC CTC ACC TGT CGA TCC TGC AAG CTC TTC TTT CGA CCG AGC GTT 480
 Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
 145 150 155 160

ACC AAG AGC GCC CTC TAC TGC TGC AAG TTC GGG CCG GCC TGC GAA ATC 528
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
 165 170 175

GAC ATC TAC ATC AGG CGA AAG TGT CAG GAG TGC CCG CTC AAA AAG TGC 576
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
 180 185 190

CTC GCC CTC GGT ATC CCG CCG GAA TCC CTC CTC CCG GAG AAC CAA TGT 624
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205

CGC ATC AAG CCG CCG GAA AAG AAG GCC CAG AAG GAG AAG GAC AAA ATC 672
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220

ACC ACT TCC CCG AGC TCT CAG CAT GCC CCG AAT GCC AGC TTC GCC TCT 720
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
 225 230 235 240

GGT GCC GCC CAA GAC TTT GTT AAG AAG GAG ATT CTT GAC CTT ATC ACA 768
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255

TCC GAG CCG CCG CAG CAT GCC ACT ATT CCG CTA CTA CCT GAT GAA ATA 816
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

TTG GCC AAG TGT CAA CCG CCG AAT ATA CCT TCC TTA ACG TAC AAT CAG 864
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

TTC GCC GTT ATA TAC AAG TTA ATT TGC TAC CAG GAT GCC TAT CAG CAG 912
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

CCA TCT GAA GAG GAT CTC AGG CGT ATA ATC AGT CAA CCG GAT CAG AAC 960
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

GAG AGC CAA ACC GAC CTC AGC TTT CCG CAT ATA ACC GAG ATA ACC ATA 1008
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

CTC ACC CTC CAG TTG ATT GTT CAG TTT GCT AAA GGT CTA CCA CCG TTT 1056
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350

ACA AAG ATA CCC CAG GAG GAG CAG ATC ACC TTA CTA AAG CCC TCC TCC 1104
 Thr Lys Ile Pro Gln Gln Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

TCC CAG GTG ATG ATG CTG CGT ATG GCA CGA CCC TAT GAC CAC AGC TCC 1152
 Ser Gln Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

GAC TCA ATA TTC TTC CCG AAT AAT AGA TCA TAT ACC CGG GAT TCT TAC 1200
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

AAA ATG CCC GGA ATG GCT GAT AAC ATT GAA GAC CTG CTG CAT TTC TCC 1248
 Lys Met Ala Gly Met Ala Asp Asn Ile Gln Asp Leu Leu His Phe Cys
 405 410 415

CGC CAA ATG TTC TCC ATG AAG CTG GAC AAC CTC GAA TAC CGC CTT CTC 1296
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Gln Tyr Ala Leu Leu
 420 425 430

ACT GCC ATT CTG ATC TTC TCC GAC CCG CCG GCG CTG GAG AAG GCC CAA 1344
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Gln Lys Ala Gln
 435 440 445

CTA CTC GAA CCG ATC CAG AGC TAC TAC ATC CAC AGC CTA CGC ATT TAT 1392
 Leu Val Gln Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

ATA CTC AAC CCC CAC TCC GCG GAC TCA ATG AGC CTC CTC TTC TAC GCA 1440
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

AAG CTC CTC TCC ATC CTC ACC GAG CTC CCT ACC CTC GGC AAC CAG AAC 1488
 Lys Leu Leu Ser Ile Leu Thr Gln Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

GCC GAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CCG AAA CTC CCC AAG 1536
 Ala Gln Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

TTC CTC GAG GAG ATC TCG GAC GTT CAT GCC ATC CCG CCA TCG CTC CAG 1584
 Phe Leu Gln Gln Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

TCC CAC CTT CAG ATT ACC CAG GAG GAG AAC GAG CGT CTC GAG CCG GCT 1632
 Ser His Leu Gln Ile Thr Gln Gln Gln Asn Gln Arg Leu Gln Arg Ala
 530 535 540

GAG CGT ATG CCG GCA TCG GTT GGG GCG GCC ATT ACC GCC GCG ATT GAT 1680
 Gln Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

TGC GAC TCT GCC TCC ACT TCC GCG GCG GCA GCC GCG GCC CAG CAT CAG 1728
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
 565 570 575

CCT CAG CCT CAG CCC CAG CCC CAA CCC TCC TCC CTC ACC CAG AAC GAT 1776
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590

TCC CAG CAG CAG ACA CAG CCG CAG CTA CAA CCT CAG CTA CCA CCT CAG 1824
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605

CTC CAA GGT CAA CTC CAA CCC CAG CTC CAA CCA CAG CTT CAG ACC CAA 1872
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCC CTC TCC GCT 1920
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640

CCC CTC CCC CCC TCC CTA ACC GCA CCT GGT TCC TTG TCC CCG CTC AGT 1968
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655

ACC ACC ACC CAA TAC ATG CCG GCA ACT CCG CCC ATA CCA CCC ATC ACC 2016
 Thr Ser Ser Gln Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670

CCG GCA ACC ACC ACC AGT ATC ACC GCT CCC GTT ACC GCT ACC TCC ACC 2064
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685

ACA TCA CCG CTA CCG ATG CCG AAC CCA GTT CCA CTC GGT GTT CCG CTC 2112
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val
 690 695 700

GGC GGC AAC CTC ACC ATG TAT CCG AAC CCG CAG ACC CCG ATG CCG TTG 2160
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720

ATG GGT CTA CCG CTC CAT TCG CAC CAA CAG CAG CTT ATC GCG GCA CTC 2208
 Met Gly Val Ala Leu His Ser His Gln Gln Gln Leu Ile Gly Gly Val
 725 730 735

GGC GTT AAG TCG GAG CAC TCG ACC ACT GCA TAG 2241
 Ala Val Lys Ser Gln His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
130 135 140

Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val
145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
165 170 175

Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys
180 185 190

Leu Ala Val Gly Met Arg Pro Gln Cys Val Val Pro Glu Asn Gln Cys
195 200 205

Ala Met Lys Arg Arg Gln Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
210 215 220

Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
225 230 235 240

Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
245 250 255

Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
260 265 270

Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
275 280 285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Gln Gln
290 295 300

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
305 310 315 320

Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
325 330 335

Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
340 345 350

Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
355 360 365

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
370 375 380

Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
385 390 395 400

Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
405 410 415

Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
420 425 430

Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
435 440 445

Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
450 455 460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
465 470 475 480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
485 490 495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
500 505 510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
545 550 555 560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln
565 570 575

Pro Gln Pro Gln Pro Gln Pro Glu Pro Ser Ser Leu Thr Gln Asn Asp
580 585 590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln

595 600 605
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2241
- (D) OTHER INFORMATION: /product= "VpEcR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GCC CCC CCG ACC GAT CTC AGC CTG GCG GAC GAG CTC CAC TTA GAC 48
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GCG GAC GAC CTG CCG ATG CCG CAT GCG GAC CCG CTA GAC GAT TTC GAT 96
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

CTG GAC ATG TTG GGG CAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC 144
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

CAC GAC TCC GCC CCG TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT 192
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

GAG CAG ATG TTT ACC GAT GCC CTT GCA ATT GAC GAG TAC CGT GGG AAG 240
 Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
 65 70 75 80

CTT CTA GGT ACC TCT AGA AGG ATA TCG AAT TCT ATA TCT TCA GGT CCG 288
 Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

GAT GAT CTC TCG CCT TCG AGC AGC TTG AAC GGA TAC TCG CGC AAC GAA 336
 Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
 100 105 110

ACC TGC GAT CGC AAG AAG ACC AAG AAG GGA CTT CGC CCA CCG CTC CAA 384
 Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
 115 120 125

GAG GAG CTC TGC CTC GTT TGC GGC CAC AGC GCC TCC GCG TAC CAC TAC 432
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

AAC GCC CTC ACC TGT GAG GCC TGC AAG GCG TTC TTT CGA CCG AGC GTT 480
 Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
 145 150 155 160

ACG AAG AGC GCC CTC TAC TGC TGC AAG TTC GCG CGC GCC TCC GAA ATG 528
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met
 165 170 175

GAC ATG TAC ATG AGC CGA AAG TGT CAG GAG TCC CGC CTC AAA AAG TCC 576
 Asp Met Tyr Met Arg Arg Lys Cys Glu Glu Cys Arg Leu Lys Lys Cys
 180 185 190

CTG GCC CTC GGT ATG CCG CCG GAA TGC CTC CTC CCG GAG AAC CAA TGT 624
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys
 195 200 205

GCG ATG AAG CCG CCG GAA AAG AAG GCC CAG AAG GAG AAG GAC AAA ATG 672
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met
 210 215 220

ACC ACT TCG CCG AGC TCT CAG CAT GCC GCG AAT GCC AGC TTC GCC TCT 720
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser
 225 230 235 240

GGT GCC GCC CAA GAC TTT GTT AAG AAG GAG ATT CTT GAC CTT ATG ACA 768
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr
 245 250 255

TGC CAG CCG CCC CAG CAT GCG ACT ATT CCG CTA CTA CCT GAT GAA ATA 816
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile
 260 265 270

TTG GCC AAG TGT CAA GCG CCG AAT ATA CCT TCC TTA ACC TAC AAT CAG 864
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln
 275 280 285

TTG GCC GTT ATA TAC AAG TTA ATT TCG TAC CAG GAT GCG TAT GAG CAG 912
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln
 290 295 300

CCA TCT GAA CAG GAT CTC AGG CGT ATA ATC ACT CAA CCC GAT GAG AAC 960
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn
 305 310 315 320

GAG AGC CAA ACG CAC GTC AGC TTT CCG CAT ATA ACC CAG ATA ACC ATA 1008
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile
 325 330 335

CTC ACG CTC CAG TTC ATT GTT CAG TTT GGT AAA GGT CTA CCA GCG TTT 1056
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe
 340 345 350

ACA AAG ATA CCC CAG CAG GAC CAG ATC ACG TTA CTA AAG GCG TCG TCG 1104
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser
 355 360 365

TCG CAG CTC ATG ATG CTC CGT ATG GCA CCA CCG TAT GAC CAC AGC TCG 1152
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380

GAC TCA ATA TTC TTC CCG AAT AAT ACA TCA TAT ACG CCG GAT TGT TAC 1200
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400

AAA ATG CCG GGA ATG GCT GAT AAC ATT GAA CAC CTC CTC CAT TTC TCG 1248
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415

CCG CAA ATG TTC TCG ATG AAG CTC GAC AAC GTC GAA TAC CCG CTT CTC 1296
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430

ACT GCC ATT CTC ATC TTC TCG GAC CCG CCG GCG CTC GAG AAG GCG CAA 1344
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
 435 440 445

CTA CTC GAA CCG ATC CAG AGC TAC TAC ATC GAC ACG CTA CCG ATT TAT 1392
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460

ATA CTC AAC CCG CAC TCG CCG GAC TCA ATG AGC CTC CTC TTC TAC CCA 1440
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480

AAG CTC CTC TCG ATC CTC ACC GAG CTC CGT ACG CTC GGC AAC CAG AAC 1488
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495

GCC GAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CCG AAA CTG CCG AAG 1536
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510

TTC CTC GAG GAG ATC TGG GAG GTT CAT GCC ATC CCG CCA TCG CTC CAG 1584
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525

TCG CAC CTT CAG ATT ACC CAG GAG GAG AAC CAG CGT CTC GAG CCG GCT 1632
 Ser His Leu Glu Ile Thr Gln Glu Glu Asn Glu Arg Leu Gln Arg Ala
 530 535 540

GAG CGT ATC CCG GCA TCG GTT CCG GCG GCC ATT ACC GCC GCG ATT CAT 1680
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560

TGC GAG TCT GCC TCC ACT TCG CCG GCG GCA GCC CCG GCC CAG CAT CAG 1728
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
 565 570 575

CCT CAG CCT CAG CCG CAG CCG CAA CCG TCC TCC CTC ACC CAG AAC GAT 1776
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590

TCC CAG CAG CAG ACA CAG CCG CAG CTA CAA CCT CAG CTA CCA CCT CAG 1824
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605

CTC CAA GGT CAA CTC CAA CCG CAG CTC CAA CCA CAG CTT CAG ACC CAA 1872
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCG CTC TCC GCT 1920
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640

CCC CTC CCG GCG TCC GTA ACC GCA CCT GGT TCC TTC TCC GCG CTC ACT 1968
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655

ACG AGC AGC CAA TAC ATG GCG GCA AGT CCG GCG ATA GGA CCC ATC ACG 2016
 Thr Ser Ser Gln Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670

CCG GCA ACC ACC AGC AGT ATC ACG GCT CCG GTT ACC GCT ACC TCC ACC 2064
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
 675 680 685

ACA TCA CCG GTA CCG ATG GCG AAC GCA CTT GCA CTC GGT GTT GCG CTC 2112
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
 690 695 700

GGC GGC AAC CTC ACC ATG TAT GCG AAC GCG CAG ACC GCG ATG GCG TTG 2160
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
 705 710 715 720

ATG CGT GTA GCC CTC CAT TCG CAC CAA CAG CAG CTT ATC GCG GGA CTC 2208
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
 725 730 735

GCG GTT AAG TCG CAG CAC TCG ACC ACT GCA TAG 2241
 Ala Val Lys Ser Glu His Ser Thr Thr Ala
 740 745

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
 115 120 125

Glu Gln Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr
 130 135 140

Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met

165	170	175
Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys		
180	185	190
Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys		
195	200	205
Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Gln Lys Asp Lys Met		
210	215	220
Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser		
225	230	235
Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr		
245	250	255
Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile		
260	265	270
Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln		
275	280	285
Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln		
290	295	300
Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn		
305	310	315
Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile		
325	330	335
Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe		
340	345	350
Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser		
355	360	365
Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser		
370	375	380
Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr		
385	390	395
Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys		
405	410	415
Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu		
420	425	430
Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln		
435	440	445
Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr		
450	455	460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
465 470 475 480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
485 490 495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
500 505 510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
545 550 555 560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
565 570 575

Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
580 585 590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
595 600 605

Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
610 615 620

Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
625 630 635 640

Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
645 650 655

Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
660 665 670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
675 680 685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
690 695 700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
705 710 715 720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
725 730 735

Ala Val Lys Ser Glu His Ser Thr Thr Ala
740 745

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..3126
 (D) OTHER INFORMATION: /product= "GECR"

(iv) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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ATG CAC TCC AAA GAA TCA TTA ACT CCT GGT AGA GAA GAA AAC CCC AGC   48
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
  1      5      10      15

ACT CTC CTT GCT CAG CAG AGG CGA GAT CTC ATG CAC TTC TAT AAA ACC   96
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
  20      25      30

CTA AGA GGA CGA GCT ACT CTC AAG GTT TCT CCG TCT TCA CCC TCA CTC   144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
  35      40      45

GCT CTC GCT TCT CAA TCA GAC TCC AAG CAG CGA AGA CTT TTG GTT GAT   192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
  50      55      60

TTT CCA AAA GGC TCA CTA AGC AAT GCG CAG CAG CCA GAT CTC TCC AAA   240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
  65      70      75      80

GCA GTT TCA CTC TCA ATG GGA CTC TAT ATG CGA CAG ACA GAA ACA AAA   288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
  85      90      95

CTC ATG CGA AAT CAC CTC GGA TTC CCA CAG CAG GGC CAA ATC AGC CTT   336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
  100     105     110

TCC TCG GGC GAA ACA GAC TTA AAG CTT TTG GAA GAA AGC ATT GCA AAC   384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Ser Ile Ala Asn
  115     120     125

CTC AAT AGC TCG ACC ACT GTT CCA GAG AAC CCC AAG ACT TCA GCA TCC   432
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
  130     135     140

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ACT GCT GTG TCT GCT GCC CCC ACA GAG AAG GAG TTT CCA AAA ACT CAC 480
 Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
 145 150 155 160

TCT GAT GTA TCT TCA GAA CAG CAA CAT TTG AAG GCC CAG ACT GCC ACC 528
 Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
 165 170 175

AAC GGT GGC AAT GTG AAA TTG TAT ACC ACA GAG CAA AGC ACC TTT GAC 576
 Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
 180 185 190

ATT TTG CAG GAT TTG GAG TTT TCT TCT GGG TCC CCA GGT AAA GAG ACG 624
 Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
 195 200 205

AAT GAG AGT CCT TGG ACA TCA CAC CTG TTG ATA GAT CAA AAC TGT TTG 672
 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
 210 215 220

CTT TCT CCT CTG GCC GGA GAA GAC GAT TCA TTC CTT TTG GAA GGA AAC 720
 Leu Ser Pro Leu Ala Gly Gln Asp Asp Ser Phe Leu Leu Glu Gly Asn
 225 230 235 240

TCC AAT GAG CAG TGC AAG CCT CTC ATT TTA CCG GAC ACT AAA CCC AAA 768
 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
 245 250 255

ATT AAG GAT AAT GGA GAT CTC GTT TTG TCA AGC CCC AGT AAT GTA ACA 816
 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
 260 265 270

CTC CCC CAA GTG AAA ACA GAA AAA CAA CAT TTG ATC GAA CTC TGC ACC 864
 Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
 275 280 285

CCT GGG GTA ATT AAG CAA GAG AAA CTG GCC ACA GTT TAC TGT CAG GCA 912
 Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
 290 295 300

AGC TTT CCT GGA GCA AAT ATA ATT GGT AAT AAA ATG TCT GCC ATT TCT 960
 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
 305 310 315 320

GTT CAT GGT GTG AGT ACC TCT GGA GCA CAG ATG TAC CAC TAT GAC ATG 1008
 Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
 325 330 335

AAT ACA GCA TCC CTT TCT CAA CAG CAG CAT CAG AAG CCT ATT TTT AAT 1056
 Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
 340 345 350

GTC ATT CCA CCA ATT CCC GTT GGT TCC GAA AAT TGC AAT AGG TGC CAA 1104
 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
 355 360 365

CGA TCT GCA GAT GAC AAC TTG ACT TCT CTG GGG ACT CTG AAC TTC CCT 1152
Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
370 375 380

GGT CGA ACA GTT TTT TCT AAT GGC TAT TCA AGC CCC AGC ATG ACA CCA 1200
Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385 390 395 400

GAT CTA AGC TCT CCT CCA TCC AGC TCC TCA ACA GCA ACA ACA GGA CCA 1248
Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro
405 410 415

CCT CCC AGC GGC CCC CTC CAA GAG GAG CTG TCC CTC GTT TGC GGC CAC 1296
Pro Pro Ser Gly Arg Val Gln Glu Leu Cys Leu Val Cys Gly Asp
420 425 430

AGG GCC TCC GGC TAC CAC TAC AAC GCC CTC ACE TGT GGA TCC TGC AAG 1344
Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys
435 440 445

GTG TTC TTT CCA CCC AGC GTT ACC AAG AGC GCC CTC TAC TGC TGC AAG 1392
Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys
450 455 460

TTC GGC GGC GGC TGC CAA ATG CAC ATG TAC ATG AGC CGA AAG TGT CAG 1440
Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln
465 470 475 480

GAG TGC CCC CTC AAA AAG TGC CTC GCC CTC GGT ATG CCC GCG GAA TGC 1488
Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys
485 490 495

GTG CTC CCG GAG AAC CAA TGT CGC ATG AAG CCG CCG GAA AAG AGC 1536
Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala
500 505 510

CAG AAG GAG AAG GAC AAA ATG ACC ACT TCG CCG AGC TGT CAG CAT GGC 1584
Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly
515 520 525

GCC AAT GGC AGC TTG GCC TCT GGT GGC GGC CAA GAC TTT GTT AAG AAG 1632
Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys
530 535 540

GAG ATT CTT GAC CTT ATG ACA TGC GAG CCG CCG CAG CAT GCC ACT ATT 1680
Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile
545 550 555 560

CCG CTA CTA CCT GAT GAA ATA TTG GCC AAG TGT CAA CCG CCG AAT ATA 1728
Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile
565 570 575

CCT TCC TTA ACC TAC AAT CAG TTG GCC GTT ATA TACAAG TTA ATT TGC 1776
Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp
580 585 590

TAC CAG GAT GGC TAT CAG CAG CCA TCT GAA GAG CAT CTC AGG CGT ATA 1824
 Tyr Gln Asp Gly Tyr Gln Gln Pro Ser Gln Gln Asp Leu Arg Arg Ile
 595 600 605

ATG AGT CAA CCC GAT CAG AAC GAG AGC CAA ACG GAC CTC AGC TTT CCG 1872
 Met Ser Gln Pro Asp Gln Asn Gln Ser Gln Thr Asp Val Ser Phe Arg
 610 615 620

CAT ATA ACC GAG ATA ACC ATA CTC ACC GTC CAG TTC ATT GTT GAG TTT 1920
 His Ile Thr Gln Ile Thr Ile Leu Thr Val Gln Leu Ile Val Gln Phe
 625 630 635 640

GCT AAA GGT CTA CCA GCG TTT ACA AAG ATA CCC CAG CAG GAC CAG ATC 1968
 Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Gln Asp Gln Ile
 645 650 655

ACC TTA CTA AAG GCG TCG TCG TCG CAG CTC ATC ATC CTC CCG ATG GCA 2016
 Thr Leu Leu Lys Ala Cys Ser Ser Gln Val Met Met Leu Arg Met Ala
 660 665 670

CGA CCG TAT CAC CAC AGC TCG CAC TCA ATA TTC TTC GCG AAT AAT AGA 2064
 Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg
 675 680 685

TCA TAT ACC CCG GAT TCT TAC AAA ATG GCG GGA ATG GCT GAT AAC ATT 2112
 Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile
 690 695 700

GAA GAC CTC CTC CAT TTC TCG CCG CAA ATG TTC TCG ATG AAG CTC GAC 2160
 Gln Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp
 705 710 715 720

AAC CTC GAA TAC GCG CTT CTC ACT GCG ATT CTC ATC TTC TCG CAC CCG 2208
 Asn Val Gln Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg
 725 730 735

CCG GCG CTC GAG AAG GCG CAA CTA CTC GAA GCG ATC CAG ACC TAC TAC 2256
 Pro Gly Leu Gln Lys Ala Gln Leu Val Gln Ala Ile Gln Ser Tyr Tyr
 740 745 750

ATC GAC ACC CTA CCG ATT TAT ATA CTC AAC CCG CAC TCG GCG GAC TCA 2304
 Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser
 755 760 765

ATG AGC CTC CTC TTC TAC GCA AAG CTC CTC TCG ATC CTC ACC GAG CTC 2352
 Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Gln Leu
 770 775 780

CGT ACC CTC GCG AAC CAG AAC GCG GAG ATG TGT TTC TCA CTA AAG CTC 2400
 Arg Thr Leu Gly Asn Gln Asn Ala Gln Met Cys Phe Ser Leu Lys Leu
 785 790 795 800

AAA AAC CCG AAA CTC CCG AAG TTC CTC GAG GAG ATC TCG GAC GTT CAT 2448
 Lys Asn Arg Lys Leu Pro Lys Phe Leu Gln Gln Ile Trp Asp Val His
 805 810 815

GCC ATC CCG CCA TCG CTC CAG TCG CAC CTT CAG ATT ACC CAG CAG CAG 2496
Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Gln Gln
820 825 830

AAC CAG CCG CTC CAG CCG GGT CAG CCG ATC CCG CCA TCG GTT GCG GCG 2544
Asn Gln Arg Leu Gln Arg Ala Gln Arg Met Arg Ala Ser Val Gly Gly
835 840 845

GCC ATT ACC GCG GCG ATT GAT TCC CAC TCT GCG TCC ACT TCG GCG GCG 2592
Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
850 855 860

GCA GCG GCG GCG CAG CAT CAG CCG CCG CAG CCG CCG CAA CCG 2640
Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
865 870 875 880

TCC TCC CTC ACC CAG AAC GAT TCC CAG CAC CAG ACA CAG CCG CAG CTA 2688
Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
885 890 895

CAA CCG CAG CTA CCA CCG CAG CTC CAA GGT CAA CTC CAA CCG CAG CTC 2736
Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
900 905 910

CAA CCA CAG CTT CAG ACC CAA CTC CAG CCA CAG ATT CAA CCA CAG CCA 2784
Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
915 920 925

CAG CTC CTT CCG CTC TCC GGT CCG CTC CCG GCG TCC CTA ACC CCA CCG 2832
Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
930 935 940

GGT TCC TTG TCC CCG CTC ACT ACC AGC AGC GAA TAC ATG GCG GGA ACT 2880
Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Gln Tyr Met Gly Gly Ser
945 950 955 960

GCG GCG ATA GGA CCG ATC ACC CCG GCA ACC ACC AGC AGT ATC ACC GGT 2928
Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
965 970 975

GCG GTT ACC GGT ACC TCC ACC ACA TCA CCG CTA CCG ATG GCG AAC GGA 2976
Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
980 985 990

GTT GGA CTC GGT GTT GCG GTC GCG GCG AAC CTC AGC ATG TAT GCG AAC 3024
Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
995 1000 1005

GCG CAG ACC GCG ATG GCG TTG ATG GGT CTA GCG CTC CAT TCG CAG CAA 3072
Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
1010 1015 1020

GAG CAG CTT ATC GCG GGA CTC GCG GTT AAG TCG CAG CAC TCG ACC ACT 3120
Gln Gln Leu Ile Gly Gly Val Ala Val Lys Ser Gln His Ser Thr Thr
1025 1030 1035 1040

GCA TAG
Ala

3126

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1041 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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Met Asp Ser Lys Gln Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
 1      5      10     15

Ser Val Leu Ala Gln Gln Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
 20     25     30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 35     40     45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
 50     55     60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
 65     70     75     80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
 85     90     95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100    105    110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115    120    125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130    135    140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145    150    155    160

Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165    170    175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
180    185    190

De Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
195    200    205

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Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
210 215 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225 230 235 240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
245 250 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
260 265 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
275 280 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
290 295 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305 310 315 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
325 330 335

Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn
340 345 350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
355 360 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
370 375 380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385 390 395 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro
405 410 415

Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp
420 425 430

Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys
435 440 445

Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys
450 455 460

Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln
465 470 475 480

Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys
485 490 495

Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala
500 505 510

Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly
515 520 525

Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys
530 535 540

Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile
545 550 555 560

Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile
565 570 575

Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp
580 585 590

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile
595 600 605

Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg
610 615 620

His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe
625 630 635 640

Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile
645 650 655

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala
660 665 670

Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg
675 680 685

Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile
690 695 700

Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp
705 710 715 720

Asn Val Gln Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg
725 730 735

Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr
740 745 750

Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser
755 760 765

Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu
770 775 780

Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu
785 790 795 800

Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His
805 810 815

Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu
820 825 830

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly
835 840 845

Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
850 855 860

Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
865 870 875 880

Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
885 890 895

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
900 905 910

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
915 920 925

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
930 935 940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
945 950 955 960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
965 970 975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
980 985 990

Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
995 1000 1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
1010 1015 1020

Gln Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
1025 1030 1035 1040

Ala

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"
/note= "N at position 7 is 0 up to 5 nucleotides, with 1 nucleotide being especially preferred."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

RCBNNMNTGN NCY

13

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"
/note= "N at position 7 can be 0 up to 5 nucleotides, with 1 nucleotide being preferred."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

RCNNCANKNN VCY

13

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGTGCANTGT TCT

13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Ecdysone Response Element"
- /note= "N at position 7 can be 0 up to 5 nucleotides, with 3 nucleotides being preferred."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

RCBNNHNRCB NNM

13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACAACGCC TCACCTGTGG ATCTGCAAG GTCTTTCTTT CCACGCAGC

49

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTACTCCCC GCGCGGCGTA TCGCGGCGCG GCCTAATCG TAGCGCGCGG GCA 53

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTACTCCCC GCGCGTAGCG ATTAGCGCG CCGCCATAG CCGCGCGCG GCA 53

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGATCG ACAAGTCAT TGTTCITTCG TGA 34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(c) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCTTTCACC AAGACAACAA TGCATTGTC CATCG